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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/479,856DATE: 02/01/2000  
TIME: 11:18:03

Input Set: I479856.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>
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ENTERED

1 <110> APPLICANT: Gross, Jane A.  
2 Xu, Wenfeng  
3 Madden, Karen  
4 Yee, David P.  
5 <120> TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING  
6 <130> FILE REFERENCE: 98-75  
7 <140> CURRENT APPLICATION NUMBER: US/09/479,856  
8 <141> CURRENT FILING DATE: 2000-01-07  
9 <150> EARLIER APPLICATION NUMBER: 60/115,068  
10 <151> EARLIER FILING DATE: 1999-01-07  
11 <150> EARLIER APPLICATION NUMBER: 60/169,890  
12 <151> EARLIER FILING DATE: 1999-12-09  
13 <160> NUMBER OF SEQ ID NOS: 60  
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
15 <210> SEQ ID NO 1  
16 <211> LENGTH: 1192  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Homo sapiens  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (6)...(746)  
22 <400> SEQUENCE: 1

23	gagta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg agc cgt gtg	50
24	Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val	
25	1 5 10 15	
26	gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag	98
27	Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys	
28	20 25 30	
29	ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt	146
30	Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys	
31	35 40 45	
32	gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg	194
33	Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg	
34	50 55 60	
35	agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa	242
36	Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu	
37	65 70 75	
38	gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac	290
39	Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His	
40	80 85 90 95	
41	aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca	338
42	Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala	
43	100 105 110	
44	gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc	386

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45      Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala
46              115                      120                      125
47      gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg      434
48      Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg
49              130                      135                      140
50      ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg      482
51      Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro
52              145                      150                      155
53      gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc      530
54      Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser
55      160                      165                      170                      175
56      aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc      578
57      Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys
58              180                      185                      190
59      agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc      626
60      Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro
61              195                      200                      205
62      act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag      674
63      Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln
64              210                      215                      220
65      cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct      722
66      Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
67              225                      230                      235
68      gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg aaaggaggag      776
69      Ala Gln Glu Gly Gly Pro Gly Ala
70      240                      245
71      ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga gagagatatg      836
72      aggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gaggagagaga      896
73      gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaga ggcagagaag      956
74      gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga      1016
75      gaggagacaga gagagataga gcaggaggtc ggggcactct gagtcccagt tcccagtgca      1076
76      gctgtaggtc gtcacacct aaccacacgt gcaataaagt cctcgtgcct gctgctcaca      1136
77      gcccccgaga gcccctctc ctggagaata aaacctttgg cagctgcct tcctca      1192
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79      <211> LENGTH: 247
80      <212> TYPE: PRT
81      <213> ORGANISM: Homo sapiens
82      <400> SEQUENCE: 2
83      Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
84      1                      5                      10                      15
85      Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
86              20                      25                      30
87      Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
88              35                      40                      45
89      Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
90              50                      55                      60
91      Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
92      65                      70                      75                      80
93      Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
94              85                      90                      95

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95 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp  
96 100 105 110  
97 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val  
98 115 120 125  
99 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly  
100 130 135 140  
101 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala  
102 145 150 155 160  
103 Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr  
104 165 170 175  
105 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg  
106 180 185 190  
107 Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr  
108 195 200 205  
109 Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro  
110 210 215 220  
111 Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala  
112 225 230 235 240  
113 Gln Glu Gly Gly Pro Gly Ala  
114 245

&lt;210&gt; SEQ ID NO 3

&lt;211&gt; LENGTH: 360

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)...(360)

&lt;400&gt; SEQUENCE: 3

123 atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg agc cgt gtg gac 48  
124 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
125 1 5 10 15  
126 cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc 96  
127 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe  
128 20 25 30  
129 tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga 144  
130 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly  
131 35 40 45  
132 cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192  
133 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser  
134 50 55 60  
135 cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240  
136 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val  
137 65 70 75 80  
138 gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288  
139 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg  
140 85 90 95  
141 ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat 336  
142 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp  
143 100 105 110  
144 cag gtg gcc ctg gtc tac agc acg 360

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145      Gln Val Ala Leu Val Tyr Ser Thr
146              115                      120
147 <210> SEQ ID NO 4
148 <211> LENGTH: 120
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
151 <400> SEQUENCE: 4
152      Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
153              1              5              10              15
154      Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
155              20              25              30
156      Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
157              35              40              45
158      Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
159              50              55              60
160      Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
161              65              70              75              80
162      Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
163              85              90              95
164      Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
165              100             105             110
166      Gln Val Ala Leu Val Tyr Ser Thr
167              115                      120
168 <210> SEQ ID NO 5
169 <211> LENGTH: 1377
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (14)...(895)
175 <400> SEQUENCE: 5
176      agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg      49
177              Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
178              1              5              10
179      agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg      97
180      Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
181              15              20              25
182      gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg      145
183      Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
184              30              35              40
185      ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc      193
186      Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
187              45              50              55              60
188      acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc      241
189      Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
190              65              70              75
191      aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc      289
192      Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
193              80              85              90
194      tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc      337

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195	Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu	
196	95 100 105	
197	agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga	385
198	Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly	
199	110 115 120	
200	gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag	433
201	Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu	
202	125 130 135 140	
203	cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481
204	His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	
205	145 150 155	
206	gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529
207	Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	
208	160 165 170	
209	gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577
210	Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	
211	175 180 185	
212	agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt	625
213	Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser	
214	190 195 200	
215	ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673
216	Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val	
217	205 210 215 220	
218	agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag	721
219	Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu	
220	225 230 235	
221	tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769
222	Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp	
223	240 245 250	
224	ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817
225	Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu	
226	255 260 265	
227	cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865
228	Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val	
229	270 275 280	
230	cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa	915
W--> 231	Pro Ala Gln Glu Gly Gly Pro Gly Ala	
232	285 290	
233	ggaggagggga gagagatgga gaggagggga gagagaaaaga gaggtgggga gaggggagag	975
234	agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag	1035
235	ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagagggc	1095
236	agagaaggaa agagacagggc agagaaggag agaggcagag agggagagag gcagagagggg	1155
237	agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg	1215
238	gcactctgag tcccagttcc cagtgcagct gttaggtcgtc atcacctaac cacacgtgca	1275
239	ataaagtcct cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa	1335
240	cctttggcag ctgcccttcc tcaaaaaaaaaa aaaaaaaaaa aa	1377
241	<210> SEQ ID NO 6	
242	<211> LENGTH: 293	
243	<212> TYPE: PRT	
	<213> ORGANISM: Homo sapiens	

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I479856.RAW

Line	Error/Warning	Original Text
231	W Line data has been corrected	Pro Ala Gln Glu Gly Gly Pro Gly Ala *
332	W Line data has been corrected	Ala Arg *
333	W Invalid/Missing Amino Acid Numbering	
490	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
492	W "N" or "Xaa" used: Feature required	Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa X
494	W "N" or "Xaa" used: Feature required	Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa
508	W "N" or "Xaa" used: Feature required	atgwsnggny tnggnmgnws nmgnmngngn ggnmgnws
509	W "N" or "Xaa" used: Feature required	tggwsnytnw sntgymgnaa rgarcarggn aarttyta
510	W "N" or "Xaa" used: Feature required	athwsntgyg cnwsnathtg yggncarcay ccnaarca
511	W "N" or "Xaa" used: Feature required	aarytnmgnw snccngtnaa yytnccnccn garytnmg
512	W "N" or "Xaa" used: Feature required	garaayaayw sngayaayws nggnmgntay carggny
513	W "N" or "Xaa" used: Feature required	wsnccngcny tnccnggny naarytnwsn gcngayca
526	W "N" or "Xaa" used: Feature required	atgwsnggny tnggnmgnws nmgnmngngn ggnmgnws
527	W "N" or "Xaa" used: Feature required	tggwsnytnw sntgymgnaa rgarcarggn aarttyta
528	W "N" or "Xaa" used: Feature required	athwsntgyg cnwsnathtg yggncarcay ccnaarca
529	W "N" or "Xaa" used: Feature required	aarytnmgnw snccngtnaa yytnccnccn garytnmg
530	W "N" or "Xaa" used: Feature required	garaayaayw sngayaayws nggnmgntay carggny
531	W "N" or "Xaa" used: Feature required	wsnccngcny tnccnggny naarytnwsn gcngayca
532	W "N" or "Xaa" used: Feature required	ytnggnytn gyytnntygc ngtnytnnty tgyttyyt
533	W "N" or "Xaa" used: Feature required	aaraarmgng gngayccntg ywsntgygar ccnmgnws
534	W "N" or "Xaa" used: Feature required	aarwsnwsnc argaycaygc natggargcn ggnwsncc
535	W "N" or "Xaa" used: Feature required	gtngaracnt gywsnttytg yttyccngar tgymgngc
536	W "N" or "Xaa" used: Feature required	acnccnggna cncngaycc nacntgygcg ggnmgntg
537	W "N" or "Xaa" used: Feature required	gtnytnarc cntgyccnca yathccngay wsnggny
538	W "N" or "Xaa" used: Feature required	cargarggng gncngngc n
738	W Invalid/Missing Amino Acid Numbering	

Input Set: I479856.RAW

Line	Original Text	Corrected Data
231	Pro Ala Gln Glu Gly Gly Pro Gly Ala *	Pro Ala Gln Glu Gly Gly Pro Gly Ala
332	Ala Arg *	Ala Arg